action.

Pages 11 and 12 of the specification provide the correct sequences of the recited EST yu23d11 and yq76e12 below the corresponding H-Robo1 sequences. While the recited EST, the recited H-Robo1 sequences, SEQ ID NO:7 and SEQ ID NO:8 are all correct, the specification contains three minor errors correlating the sequence position number from the SEQ ID NOS with the recited sequences. In particular, careful examination of SEQ ID NO:8 shows that the H-Robo1 portions recited on pages 11 and 12 (which correspond to the two excluded EST translates) are residues 168-217 and 1316-1520, respectively. SEQ ID NO:7 codes for SEQ ID NO:8, so the corresponding portions of SEQ ID NO:7 are 502-651 and 3946-4560, respectively. Unfortunately, these corresponding portions of the SEQ ID NOS were not all correctly identified in the specification.

We enclose copies of pages 58, 60, 61 and 65 of the application, marked up to identify the H-Robo1 sequences recited on pages 11-12 and the corresponding coding sequences.

We apologize for the unnecessary confusion caused by the errors in our specification. We note that the amended claims were correct, that all the correct sequence data, SEQ ID NOS and provisos are properly contained in the application, that it was only three cross-references between the recited sequences and the SEQ ID NOS that were erroneous and that these amendments, correcting the cross-references, introduce no new matter.

Upon allowability of the product claims of elected Group II (claims 10-42 and 50-67), Applicants request joinder of method claims 43-49 (in the case of an elected product claim, rejoinder will be permitted when a product claim is found allowable and the withdrawn process claim depends from or otherwise includes all the limitations of an allowed product claim, per Commissioner Lehman's Notice of February 28, 1996: Guidance on Treatment of Product and Process Claims in light of In re Ochiai, In re Brouwer and 35 U.S.C. 103(b)).

Respectfully submitted,
SCIENCE & TECHNOLOGY LAW GROUP

Richard Aron Osman, Ph.D., Reg. No. 36,627
Telephone: (650) 343-4341

encl. Pages 58, 60, 61 and 65.

2   08/971,172

```
         1250              1255              1260

Ala Ser Thr Leu Ala His Ser Cys Tyr Gly Thr Asn Gly Thr Ala Gln

 1265              1270              1275              1280

Arg Phe Arg Ser Ile Pro Arg Asn Asn Gly Ile Val Thr Gln Glu Gln

              1285              1290              1295

Thr
```

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 4956 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
ATGAAATGGA AACATGTTCC TTTTTTGGTC ATGATATCAC TCCTCAGCTT ATCCCCAAAT    60
CACCTGTTTC TGGCCCAGCT TATTCCAGAC CCTGAAGATG TAGAGAGGGG GAACGACCAC   120
GGGACGCCAA TCCCCACCTC TGATAACGAT GACAATTCGC TGGGCTATAC AGGCTCCCGT   180
CTTCGTCAGG AAGATTTTCC ACCTCGCATT GTTGAACACC CTTCAGACCT GATTGTCTCA   240
AAAGGAGAAC CTGCAACTTT GAACTGCAAA GCTGAAGGCC GCCCCACACC CACTATTGAA   300
TGGTACAAAG GGGAGAGAG AGTGGAGACA GACAAAGATG ACCCTCGCTC ACACCGAATG   360
TTGCTGCCGA GTGGATCTTT ATTTTTCTTA CGTATAGTAC ATGGACGGAA AAGTAGACCT   420
GATGAAGGAG TCTATGTCTG TGTAGCAAGG AATTACCTTG AGAGGCTGT GAGCCACAAT   480
GCATCGCTGG AAGTAGCCAT ACTTCGGGAT GACTTCAGAC AAAACCCTTC GGATGTCATG   540
GTTGCAGTAG GAGAGCCTGC AGTAATGGAA TGCCAACCTC CACGAGGCCA TCCTGAGCCC   600
ACCATTTCAT GGAAGAAAGA TGGCTCTCCA CTGGATGATA AGATGAAAG AATAACTATA   660
CGAGGAGGAA AGCTCATGAT CACTTACACC CGTAAAAGTG ACGCTGGCAA ATATGTTTGT   720
GTTGGTACCA ATATGGTTGG GGAACGTGAG AGTGAAGTAG CCGAGCTGAC TGTCTTAGAG   780
AGACCATCAT TTGTGAAGAG ACCCAGTAAC TTGGCAGTAA CTGTGGATGA CAGTGCAGAA   840
TTTAAATGTG AGGCCCGAGG TGACCCTGTA CCTACAGTAC GATGGAGGAA AGATGATGGA   900
GAGCTGCCCA AATCCAGATA TGAAATCCGA GATGATCATA CCTTGAAAAT TAGGAAGGTG   960
ACAGCTGGTG ACATGGGTTC ATACACTTGT GTTGCAGAAA ATATGGTGGG CAAAGCTGAA  1020
GCATCTGCTA CTCTGACTGT TCAAGAACCT CCACATTTTG TTGTGAAACC CCGTGACCAG  1080
GTTGTTGCTT TGGGACGGAC TGTAACTTTT CAGTGTGAAG CAACCGGAAA TCCTCAACCA  1140
GCTATTTTCT GGAGGAGAGA AGGGAGTCAG AATCTACTTT TCTCATATCA ACCACCACAG  1200
TCATCCAGCC GATTTTCAGT CTCCCAGACT GGCGACCTCA CAATTACTAA TGTCCAGCGA  1260
TCTGATGTTG GTTATTACAT CTGCCAGACT TTAAATGTTG CTGGAAGCAT CATCACAAAG  1320
GCATATTTGG AAGTTACAGA TGTGATTGCA GATCGGCCTC CCCCAGTTAT TCGACAAGGT  1380
```

```
GCAAGGATGT ATTTGCAACA AGATGAATTA GAAGAGGAGG AAGATGAACG AGGCCCCACT    3720
CCCCCTGTTC GGGGAGCAGC TTCTTCTCCA GCTGCCGTGT CCTATAGCCA TCAGTCCACT    3780
GCCACTCTGA CTCCCTCCCC ACAGGAAGAA CTCCAGCCCA TGTTACAGGA TTGTCCAGAG    3840
GAGACTGGCC ACATGCAGCA CCAGCCCGAC AGGAGACGGC AGCCTGTGAG TCCTCCTCCA    3900
CCACCACGGC CGATCTCCCC TCCACATACC TATGGCTACA TTTCAGGACC CCTGGTCTCA    3960
GATATGGATA CGGATGCGCC AGAAGAGGAA GAAGACGAAG CCGACATGGA GGTAGCCAAG    4020
ATGCAAACCA GAAGGCTTTT GTTACGTGGG CTTGAGCAGA CACCTGCCTC CAGTGTTGGG    4080
GACCTGGAGA GCTCTGTCAC GGGGTCCATG ATCAACGGCT GGGGCTCAGC CTCAGAGGAG    4140
GACAACATTT CCAGCGGACG CTCCAGTGTT AGTTCTTCGG ACGGCTCCTT TTTCACTGAT    4200
GCTGACTTTG CCCAGGCAGT CGCAGCAGCG GCAGAGTATG CTGGTCTGAA AGTAGCACGA    4260
CGGCAAATGC AGGATGCTGC TGGCCGTCGA CATTTTCATG CGTCTCAGTG CCCTAGGCCC    4320
ACAAGTCCCG TGTCTACAGA CAGCAACATG AGTGCCGCCG TAATGCAGAA AACCAGACCA    4380
GCCAAGAAAC TGAAACACCA GCCAGGACAT CTGCGCAGAG AAACCTACAC AGATGATCTT    4440
CCACCACCTC CTGTGCCGCC ACCTGCTATA AAGTCACCTA CTGCCCAATC CAAGACACAG    4500
CTGGAAGTAC GACCTGTAGT GGTGCCAAAA CTCCCTTCTA TGGATGCAAG AACAGACAGA    4560
TCATCAGACA GAAAAGGAAG CAGTTACAAG GGGAGAGAAG TGTTGGATGG AAGACAGGTT    4620
GTTGACATGC GAACAAATCC AGGTGATCCC AGAGAAGCAC AGGAACAGCA AAATGACGGG    4680
AAAGGACGTG GAAACAAGGC AGCAAAACGA GACCTTCCAC CAGCAAAGAC TCATCTCATC    4740
CAAGAGGATA TTCTACCTTA TTGTAGACCT ACTTTTCCAA CATCAAATAA TCCCAGAGAT    4800
CCCAGTTCCT CAAGCTCAAT GTCATCAAGA GGATCAGGAA GCAGACAAAG AGAACAAGCA    4860
AATGTAGGTC GAAGAAATAT TGCAGAAATG CAGGTACTTG GAGGATATGA AAGAGGAGAA    4920
GATAATAATG AAGAATTAGA GGAAACTGAA AGCTGA                              4956
```

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 1651 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Met Lys Trp Lys His Val Pro Phe Leu Val Met Ile Ser Leu Leu Ser
1               5                   10                  15
Leu Ser Pro Asn His Leu Phe Leu Ala Gln Leu Ile Pro Asp Pro Glu
            20                  25                  30
Asp Val Glu Arg Gly Asn Asp His Gly Thr Pro Ile Pro Thr Ser Asp
            35                  40                  45
Asn Asp Asp Asn Ser Leu Gly Tyr Thr Gly Ser Arg Leu Arg Gln Glu
```

```
                50                          55                          60
Asp Phe Pro Pro Arg Ile Val Glu His Pro Ser Asp Leu Ile Val Ser
65                          70                          75                          80
Lys Gly Glu Pro Ala Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr
                85                          90                          95
Pro Thr Ile Glu Trp Tyr Lys Gly Gly Glu Arg Val Glu Thr Asp Lys
                100                         105                         110
Asp Asp Pro Arg Ser His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe
                115                         120                         125
Phe Leu Arg Ile Val His Gly Arg Lys Ser Arg Pro Asp Glu Gly Val
                130                         135                         140
Tyr Val Cys Val Ala Arg Asn Tyr Leu Gly Glu Ala Val Ser His Asn
145                         150                         155                         160
Ala Ser Leu Glu Val Ala Ile Leu Arg Asp Asp Phe Arg Gln Asn Pro
                165                         170                         175
Ser Asp Val Met Val Ala Val Gly Glu Pro Ala Val Met Glu Cys Gln
                180                         185                         190
Pro Pro Arg Gly His Pro Glu Pro Thr Ile Ser Trp Lys Lys Asp Gly
                195                         200                         205
Ser Pro Leu Asp Asp Lys Asp Glu Arg Ile Thr Ile Arg Gly Gly Lys
                210                         215                         220
Leu Met Ile Thr Tyr Thr Arg Lys Ser Asp Ala Gly Lys Tyr Val Cys
225                         230                         235                         240
Val Gly Thr Asn Met Val Gly Glu Arg Glu Ser Glu Val Ala Glu Leu
                245                         250                         255
Thr Val Leu Glu Arg Pro Ser Phe Val Lys Arg Pro Ser Asn Leu Ala
                260                         265                         270
Val Thr Val Asp Asp Ser Ala Glu Phe Lys Cys Glu Ala Arg Gly Asp
                275                         280                         285
Pro Val Pro Thr Val Arg Trp Arg Lys Asp Asp Gly Glu Leu Pro Lys
                290                         295                         300
Ser Arg Tyr Glu Ile Arg Asp Asp His Thr Leu Lys Ile Arg Lys Val
305                         310                         315                         320
Thr Ala Gly Asp Met Gly Ser Tyr Thr Cys Val Ala Glu Asn Met Val
                325                         330                         335
Gly Lys Ala Glu Ala Ser Ala Thr Leu Thr Val Gln Glu Pro Pro His
                340                         345                         350
Phe Val Val Lys Pro Arg Asp Gln Val Val Ala Leu Gly Arg Thr Val
```

```
1265                  1270                1275                1280
```
Glu Thr Gly His Met Gln His Gln Pro Asp Arg Arg Arg Gln Pro Val
```
                1285                1290                1295
```
Ser Pro Pro Pro Pro Pro Arg Pro Ile Ser Pro Pro His Thr Tyr Gly
```
              1300                1305                1310
```
Tyr Ile Ser Gly Pro Leu Val Ser Asp Met Asp Thr Asp Ala Pro Glu
```
              1315                1320                1325
```
Glu Glu Glu Asp Glu Ala Asp Met Glu Val Ala Lys Met Gln Thr Arg
```
            1330                1335                1340
```
Arg Leu Leu Leu Arg Gly Leu Glu Gln Thr Pro Ala Ser Ser Val Gly
```
1345                  1350                1355                1360
```
Asp Leu Glu Ser Ser Val Thr Gly Ser Met Ile Asn Gly Trp Gly Ser
```
                1365                1370                1375
```
Ala Ser Glu Glu Asp Asn Ile Ser Ser Gly Arg Ser Ser Val Ser Ser
```
              1380                1385                1390
```
Ser Asp Gly Ser Phe Phe Thr Asp Ala Asp Phe Ala Gln Ala Val Ala

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```
              1395                1400                1405
```
Ala Ala Ala Glu Tyr Ala Gly Leu Lys Val Ala Arg Arg Gln Met Gln
```
            1410                1415                1420
```
Asp Ala Ala Gly Arg Arg His Phe His Ala Ser Gln Cys Pro Arg Pro
```
1425                  1430                1435                1440
```
Thr Ser Pro Val Ser Thr Asp Ser Asn Met Ser Ala Ala Val Met Gln
```
                1445                1450                1455
```
Lys Thr Arg Pro Ala Lys Lys Leu Lys His Gln Pro Gly His Leu Arg
```
              1460                1465                1470
```
Arg Glu Thr Tyr Thr Asp Asp Leu Pro Pro Pro Pro Val Pro Pro Pro
```
              1475                1480                1485
```
Ala Ile Lys Ser Pro Thr Ala Gln Ser Lys Thr Gln Leu Glu Val Arg
```
              1490                1495                1500
```
Pro Val Val Val Pro Lys Leu Pro Ser Met Asp Ala Arg Thr Asp Arg
```
1505                  1510                1515                1520
```
Ser Ser Asp Arg Lys Gly Ser Ser Tyr Lys Gly Arg Glu Val Leu Asp
```
                1525                1530                1535
```
Gly Arg Gln Val Val Asp Met Arg Thr Asn Pro Gly Asp Pro Arg Glu
```
              1540                1545                1550
```
Ala Gln Glu Gln Gln Asn Asp Gly Lys Gly Arg Gly Asn Lys Ala Ala
```
              1555                1560                1565
```
Lys Arg Asp Leu Pro Pro Ala Lys Thr His Leu Ile Gln Glu Asp Ile

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